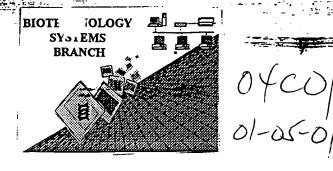
## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	09/740,288		: :
Source:	OIPE	_	•
Date Processed by STIC:	01-09-01	_ ;	

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 c-mail help: <a href="mailto:patin21help@uspto.gov">patin21help@uspto.gov</a> or phone 703-306-4119 (R. Wax) PATENTIN 3.0 c-mail help: <a href="mailto:patin30help@uspto.gov">patin30help@uspto.gov</a> or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

OIPE

 RAW SEQUENCE LISTING
 DAIL: 01/09/2001

 PATENT APPLICATION: US/09/740,288
 TIME: 13:17:05

Input Set : A:\BB1429 US NA Seq Listing.txt
Output Set: N:\CRF3\01092001\1740288.raw

```
2 <110> APPLICANT: Allen, Steve
              Kinne/, Tony
              Miao, Gou-Hua
              Orozco, Buddy
      7 <120> TITLE OF INVENTION: PLANT BIOTIN SYNTHASE
     9 <130> FILE REFERENCE: BB1429 US NA
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/740,288
C--> 12 <141> CURRENT FILING DATE: 2000-12-19
     14 <150> PRIOR APPLICATION NUMBER: 60/172929
W--> 15 <151> PRIOR FILING DATE: December 21, 1999 > /999 - /2 - 2/
     17 <160> NUMBER OF SEQ ID NOS: 36
     19 <170> SOFTWARE: Microsoft Office 97
     21 <210> SEQ ID NO: 1
     22 <211> LENGTH: 512
     23 <212> TYPE: DNA
     24 <213> ORGANISM: Hordeum vulgare
     26 <220> FEATURE:
     27 <221> NAME/KEY: unsure
     28 <222> LOCATION: (94)
     30 <220> FEATURE:
     31 <221> NAME/KEY: unsure
     32 <222> LOCATION: (460)
     34 <220> FEATURE:
     35 <221> NAME/KEY: unsure
     36 <222> LOCATION: (462)
     38 <100> SEQUENCE: 1
     39 caacteecte ggoagtateg entagtgrag cageggetee gttenggeea gettigeting
W--> 40 ccgagecgge catgatgetg etgetegege geanettege tecegegtee ggteeceett 120
     11 egeoteegee gttagegeeg egeoctinic aleggiateg geggeegegg eggaggegga 180
     42 egggegite quaegque cagqaacqae tygaccque cegaqateca gqccatetae 240
     43 gacteeege teeteyaeet eetetteeae gggqeteaag teeataggaa tgteeataaa 300
     44 titagagaag tigcaacaati cacacticti icaatawaga ciiggiiggii cagcgaagat 360
     45 tyttcatact georacagle ttoaagatac agraeeggat tyaaggetga aaaatraatg 420
W--> 46 aagaaagatg ccgtcctaga agcagctaaa aaggcaaagn angctgggag cacccgattt 480
     47 tgattggage gatggagaga gacaattgge ag
     49 <210> SEO ID NO: 2
     50 <211> LENGTH: 137
     51 <212> TYPE: PRT
     52 <213> ORGANISM: Hordeum vulgare
     54 <220> ΓΕΑΤURE:
     55 <221> NAME/KEY: UNSURE
     56 <222> LOCATION: (131)
     58 <400> SEQUENCE: 2
     59 Met Met Leu Leu Ala Arg Ser Leu Arg Ser Arg Val Arg Ser Pro
                                            10
     62 Phe Ala Ser Ala Val Ser Ala Ala Pro Phe Ser Ser Val Ser Ala Ala
                    20
```

Corrected Diskette Needed

Input Set : A:\BB1429 US NA Seq Listing.txt Output Set: N:\CRF3\01092001\I740288.raw 65 Ala Ala Glu Ala Glu Arg Ala Val Arg Asp Gly Pro Arg Asu Asp Trp 35 40 66 68 Thr Arg Pro Glu Ile Glu Ala Ile Fyr Asp Ser Pro Leu Leu Asp Leu 55 60 71 Len Phe His Gly Ala Gln Val His Arg Asn Val His Lys Phe Arg Glu 72 65 70 75 80 70 72 65 74 Val Glm Glm C/s Thr Len Leu Ser He Lvs Thr Gl/ Gly Cys Ser Glu 85 90 75 77 Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Ser Thr Glv Leu Lys 78 \$100\$ 100 \$105\$80 Ala Glu Lys Leu Met Lys Lys Asp Ala Val Leu Glu Ala Ala Lys Lys 81  $\phantom{\bigg|}$  115  $\phantom{\bigg|}$  120  $\phantom{\bigg|}$  125 W--> 83 Ala Lys Xaa'Ala Gly Ser Thr Arg Phe 84 130 86 - 210> SEQ 1D NO: 3 87 <211> LENGTH: 496 88 <212> TYPE: DNA 89 <213> ORGANISM: Zea mays 91 <220> FEATURE: 92 <221> NAME/KEY: unsure/ 93 <222> LOCATION: (33) 95 <220> FEATURE: 96 <221> NAME/KEY: unsure/ 97 <222> LOCATION: (318) 99 <220> FFATURF: 100 <221> NAME/KEY: unsure 101 <222> LOCATION: (321) 103 <220> FEATURE: 104 <221> NAME/KFY: unsure 105 <222> LOCATION: (365) 107 <220> FEATURE: 108 <221> NAME/KEY: unsure 109 <222> LOCATION: (446) 111 <100> SEQUENCE: 3 W--> 112 tecaateggg tgggeagttt ttaaggaaac canggaeege aageaageaa geegeeeeag 60 113 cogacqagge gaggayegtg caattrogta qetgeaaega acteentega cegtategee 120 114 egetgeteet etatecettt eetgetgetg etactacett aagetateac tateatggee 180 115 tigatyctgo tagogogaa notgogotoo ngootoogoo naongotogo ogoogongog 210 116 gggttetegt eggeegege ggaggegaa agggegatae gggaeggee geggaacque 300 W--> 117 tggagcegge eegagatńea ńgeegtetae gaeteaeege teetegaeet eetettteae 360 W--> 118 ggggńtcagt catcaagata caacactgga ttgaagggcc aaaaattgat gaacaaatat 420 W--> 119 gctgtcttgg gagcagcaaa aaaggńaaaa gagtctggga agcaaccgtt tttgcatggg 480 120 aactgcattg gagaaa 122 <210> SEQ TD NO: 4 123 <211> LENGTH: 102 124 <212> TYPE: PRT 125 <213> ORGANISM: Zea mays 127 <220> FEATURE: 128 <221> NAME/KEY: UNSURE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/740,288

DATE: 01/69/2001

TIME: 13:17:05

RAW SEQUENCE LISTING DATE: 01/09/2001
PATENT APPLICATION: US/09/740,288 FIME: 13:17:05

Input Set : A:\BB1429 US NA Seq Listing.txt
Ont.put Set: N:\CRF3\01092001\1740288.raw

```
129 <222> LOCATION: (48)..(49)
      131 <220> FFATURE:
      132 <221> NAME/KEY: UNSURE
      133 <222> LOCATION: (54)
     135 <220> FEATURE:
     136 <221> NAME/KEY: UNSURE /
     137 <222> LOCATION: (91)
      139 <400> SEQUENCE: 4
     110 Met Ala Leu Wet Leu Leu Ala Arg Ash Leu Arg Ser Arg Leu Arg Pro 141 \phantom{-}1\phantom{-}1\phantom{-}5\phantom{-}10\phantom{-}15\phantom{-}15\phantom{-}1
     143 Pro Leu Ala Ala Ala Ala Gly Phe Ser Ser Ala Ala Ala Glu Ala Glu l44 20 25 30 \times
W--> 146 Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Xaa 147 35 40 45 35 W--> 149 Xaa Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Xaa 150 50 50 55 60
     152 Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Gly Gln Lys Leu Bet Asn 153 -65 70 75 80
W--> 155 Lys Tyr Ala Val Leu Gly Ala Ala Lys Lys Xaa Lys Glu Ser Gly Lys
156 85 90 95
      158 Gln Pro Phe Leu His Gly
                        100
      159
      161 <210> SEQ ID NO: 5
      162 <211> LENGTH: 497
      163 <212> TYPE: DNA
      164 <213> ORGANISM: Zea mays
      166 <230> FFATURE:
      167 <221> NAME/KEY: unsure /
     168 <222> LOCATION: (192)
      170 <220> FLATURE:
      171 <221> NAME/KEY: unsure
      172 <222> LOCATION: (460) /
     174 <220> FEATURE:
     175 <221> NAME/KEY: unsure /
     176 <222> LOCATION: (463)
     178 <220> FEATURE:
      179 <221> NAME/KEY: unsure /
     180 <222> LOCATION: (469)
     182 <220> FEATURE:
     183 <221> NAME/KEY: unsure /
     184 <222> LOCATION: (490)
     186 <400> SEQUENCE: 5
     187 agooglogag gegaggageg tigeaaltoog tagotigeaac tigeaacgaac teertreete 60
     188 octogaccyt alogeocyct getretetat coettteety etyctyctae taccitaage 120
     189 Lalealgged tigalgetge tagegegeaa eetgegetee egeetengne eucegetinge 180
W--> 190 cgccgccgcg gńgttctcgt cggccgcggc ggaggcggag agggcgatac gggacgggcc 240
     191 geggaucgae tygageegge regagattea agregitetae gaetrarege heef equent 300
     192 crtc.ttrac ggggctouag tecaragaau tytecataau tteaugaqau gtgcuqeant 360
```

193 gcacuettet tteaateuag aetgytggga tgeagtgaag attyttetta etgteeteaa 420



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/740,288

DAIL: 01/09/2001

Input Set : A:\BB1429 US NA Seq Listing.txt
Output Set: N:\CRF3\01092001\1740288.raw

```
W--> 194 gtcatcaaag aatacaacac tgggattgaa gggcccaaan aanttgatna acaaaagatg 480
W--> 195 ctgtcttggn aacaaca
     197 <210> SEQ ID NO: 6
     198 <211> LENGTH: 98
     199 <212> TYPE: PRT
     200 <213> ORCANISH: Zea ma, s
     202 <220> FLATURE:
     203 <221> NAME/KEY: UNSURE,
     204 <222> LOCALION: (23)
     206 <220> FEATURE:
     207 <221> NAME/KEY: UNSURE (
     208 <222> LOCATION: (72)
     210 <220> FEAFURE:
     211 <221> NAME/KEY: UNSURE
     212 <222> LOCATION: (39)
     214 <400> SEQUENCE: 6
     215 Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro
     21.6 1
                           5
                                              10
W--> 218 Pro Leu Ala Ala Ala Ala Xaa Phe Ser Ser Ala Ala Ala Glu Ala Glu 219 20 25 30
     221 Arg Ala Ile Arg Asp Gly Pro Arg Asm Asp Prp Ser Arg Pro Glu 11e
     222 35
                                     40
224 Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
225 50 55 60
W--> 227 Gln Val His Arg Asn Val His Xaa Ser Arg Glu Val Gln Gln Cys Thr
                                                 75
                          7 U
     228 65
W--> 230 Leu Leu Ser Ile Lys Thr Gly Gly Xaa Ser Glu Asp Cys Ser Tyr Cys
     233 Pro Gin
     236 <210> SEO ID NO: 7
     237 <211> LINGTH: 1.152
     238 <212> TYPE: DNA
     239 <213> ORGANISM: Zea mays
     241 <400> SEQUENCE: 7
     242 geagergang aggegaggag ngtgeaatte ngtagetgea acgaactoon tegacogtul
     243 egeocyclyc tectotatec citteetget gotgetacta collaageta teactateut
                                                                               120
     244 ggenttgatg etgetagege geaacetgeg ethologeete egeonaenge tegeogenge
                                                                               180
     245 agoggogtto toqtoggong agganggaggo ggagaggog atangggang agongangua
     246 cgartggage cggcccgaga thraggeogt ctacquetea regeteeteg aceteetett
     247 toacqqqqct caqqtccaca qaaatqtcca Laaattcaqa qaaqtqcaqc aatqcacact
     248 tetttemate magaetygtg gatgemagtgm magattyttet tactyteete mytemtemag
                                                                               120
     249 atacaacact ggattgaagg comaaaaatt gatgaacaaa tatgotgtot tggaagcagc
                                                                               180
     250 aaaaauggca aaagagtotg ggagcacccg Lttttgcatg ggagctgcat ggagagaaac
     251 cattggcagg aaatcaaact tcaaccagat tottgaatat gtcaaggaaa taaggggtut
                                                                              660
     252 gagnatggag gtotgttgca cactaggcat gatagagaaa cuacaagnig aagaactnaa
                                                                               720
     253 quaggetigga ettacageat ataateutaa eetagataca teaagagagt attateeeaa
     254 cattattace acaugateat atgatgatag actgoagact cttgagcatg teegtgaage
                                                                               780
     255 tygaataago atotgotoag giggaatoat tygiotitggi gaagoagagg aggacogggi
     256 agggttgtig catacoctag ctaccttgcc tacacaccca gagagogttc ctattaatgc
```



PATENT APPLICATION: US/09/740,288

DA!E: 01/09/2001 PIMF: 13:17:06

Input Set : A:\BB1429 US NA Seq Listing.txt
Output Set: N:\CRF3\01092001\1740288.raw

257 uttgyttgot gladuugged carctettgd ggaccagadg cetglagaga telgggadat. 960 258 galongoatg atogecacty otoggatoac gatgecasag gesatggtga ggotttcage 1020 25% aggccqagta eggttetega tgccagadea agegetqtqc ttectegetq qqqccaacte 1080 260 natrottgoo ggogaqaaac ttotoanaac cgouaanaac gaotttgatg oggucoaago 1140 261 gatgitcaag at 263 <210> SEQ ID NO: 8 264 <211> LENGTH: 344 265 <212> TYPE: PRT 266 <213> ORGANISM: Zea mays 268 <400> SEQUENCE: 3 269 Met Ala Leu Met Leu Leu Ala Arg As<br/>n Leu Arg Ser Arg Leu Arg Pro270-1 -5 -10 -15272 Pro Leu Ala Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu 273 20 30 275 Arg Ala Ile Arg Asp Gly Pro Arg Ash Asp Trp Ser Arg Pro Glu Ile 276 35 40 278 Gln Ala Val Fyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala 279 50 55 60 281 Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr 282 65 70 75 80 282 65 287 Pro Gln Ser Ser Arg Tvr Ash Thr Gly Leu Lvs Ala Gln Lys Leu Met 288 100 105 110290 Asn Lys Tyr Ala Val Leu Giu Ala Ala Lys Lys Ala Lys Giu Ser Gly 291 115 120 125 293 Ser Thr Arg Phe Cys Met GUy Ala Ala Trp Arg Glu Thr The Gly Arg 294 130 135 140 296 Lys Ser Asn Phe Asn Gin Tie Leu Glu Tyr Val Lys Glu Ile Arg Gly 297 145 150 155 160 299 Met Gly Met Glu Val Cys Cys Thr Leu Gly Met IIe Glu Lvs Glu Gln 300 165 170 170 302 Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu 303 180 185 190 305 Asp Thr Ser Arg Glu Tyr Tyr Pro Asn lie Ile Thr Thr Arg Ser Tyr 200 205 306 195 308 Asp Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser 309 210 215 220 311 The Cys Ser Gly Gry The The Gly Leu Gly Glu Ala Glu Glu Asp Arg 312 225 230 235 240 314 Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser 315 245 250 . 255 317 Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glú Asp 318 260 265 270 318 260 320 Glm Lys Pro Val Glu Ile Trp Glu Het Ile Arg Met Ile Ala Thr Ala 321 275 280 285 323 Arg 11e Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val 324 290 295 300 326 Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn

p. 6

<210> 36 Seg # 36 <211> 12	
	sing mondatory field:
<400> 36 Gly Xaa Cys Xaa Glu Asp Cys Xaa Tyr Cys Xaa Gl 1 10	.n Zziz> organism
Missing mandatory (220), to explain "Xaa's" in the	y to (223) features e sequence.

KF.Y.I.

## Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.



VERIFICATION SUMMARY

PAIRNI APPLICATION: US/09/740,288

DATE: 01/09/2001 TIME: 13:17:07

Input Set: A:\BB1429 US NA Seq Listing.txt Output Set: N:\CRF3\01092001\1740288.raw

L:11 M:270 C: Current Application Number differs, keplaced Application Number L-12 M-271 C: Current Filing Date differs, Replaced Current Filing Date L:15 M:256 W: Invalid hameric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD 1:40 M:258 W: Mandat ry reature missing, <225> not found for SEQ ID4:1 L:40 M:34( E: (40) "n" or "Xaa" used: Feature required, for SEO ID::1 L:46 H:258 W: Mandator, Feature missing, <223> not found for SEQ ID4:1 M:340 Repeated in SegNost  $1:83~\text{M}{:}258~\text{W}{:}$  Mandatory Feature missing, <223> not found for SEQ ID#:2 E:83 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ 1D#:2 L:112 M:258 W: Mandatory Feature missing, <223> not found for SEO 1D#:3 L:112 M:340 W: (16) "n" or "Xaa" used: Feature required, for SEQ ID::3 h:117 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3 M:340 Repeated in SeqNo 3 L:118 M:258 W: Mandatory Feature missing, <223> not tound for SEQ ID#:3 L.119 M:258 %: Mandatory Feature missing, <223> not found for SEQ ID#:3 L:146 M:258 W: Mandator? Feature missing, <223> not found for SEQ ID#:4 L:146 M:340 W: (46) "n" or "Naa" used: Feature required, for SEQ ID#:4 L:149 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID\*:4 M:340 Repeated in SeqNo-4 L:155 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4 L:190 M:258 W: Mandatory Feature missing, <223> not found for SEQ 1D#:5 L:190 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5 L:194 M:258 W: Mandatory Feature missing, <223> not found for SEQ TD#:5 M:340 Repeated in SeqNo-5 L:195 M:258 W: Mandatory Feature missing, <223> not found for SEQ 1D#:5L:218 H:258 W: Handatory Feature missing, <223> not found for SEQ TD#:6 L:218 M:340 M: (46) "n" or "Xaa" used: Feature required, for SEQ IDF:6 L:227 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6 M:340 Repeated in SegNo 6 L:230 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6 Li:354~M:258~M: Handatory Feature missing, <223> not found for SEQ TD#:9 6:354 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEO IDF:9 L:586 H:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15 L:586 M:340 W: (46) "n" or "Xaa" used: Feature required, for SLO ID::15 L:587 H:258 W: Mandatory Feature missing, <223> not found for SEO TD::15 M:340 Repeated in SeqNo 15 L:589 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15 L:590 H:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15 L:614 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID::16 L:614 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16  $1:1721~\mathrm{M}:201~\mathrm{W}:$  Mandatory field data missing, ORGANISM L:1724 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:36 L:1724 M:258 W: Mandator, feature missing, <221> not found for SEQ ID#:36 L:1724 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:36 L:1724 M:258 W: Mandatory Feature missing, <223> not tound for SFO ID#:36 L:1724 H:340 W: (40) "n" or "Xaa" used: Feature required, for SEQ ID#:36